

#6



Fig. 1

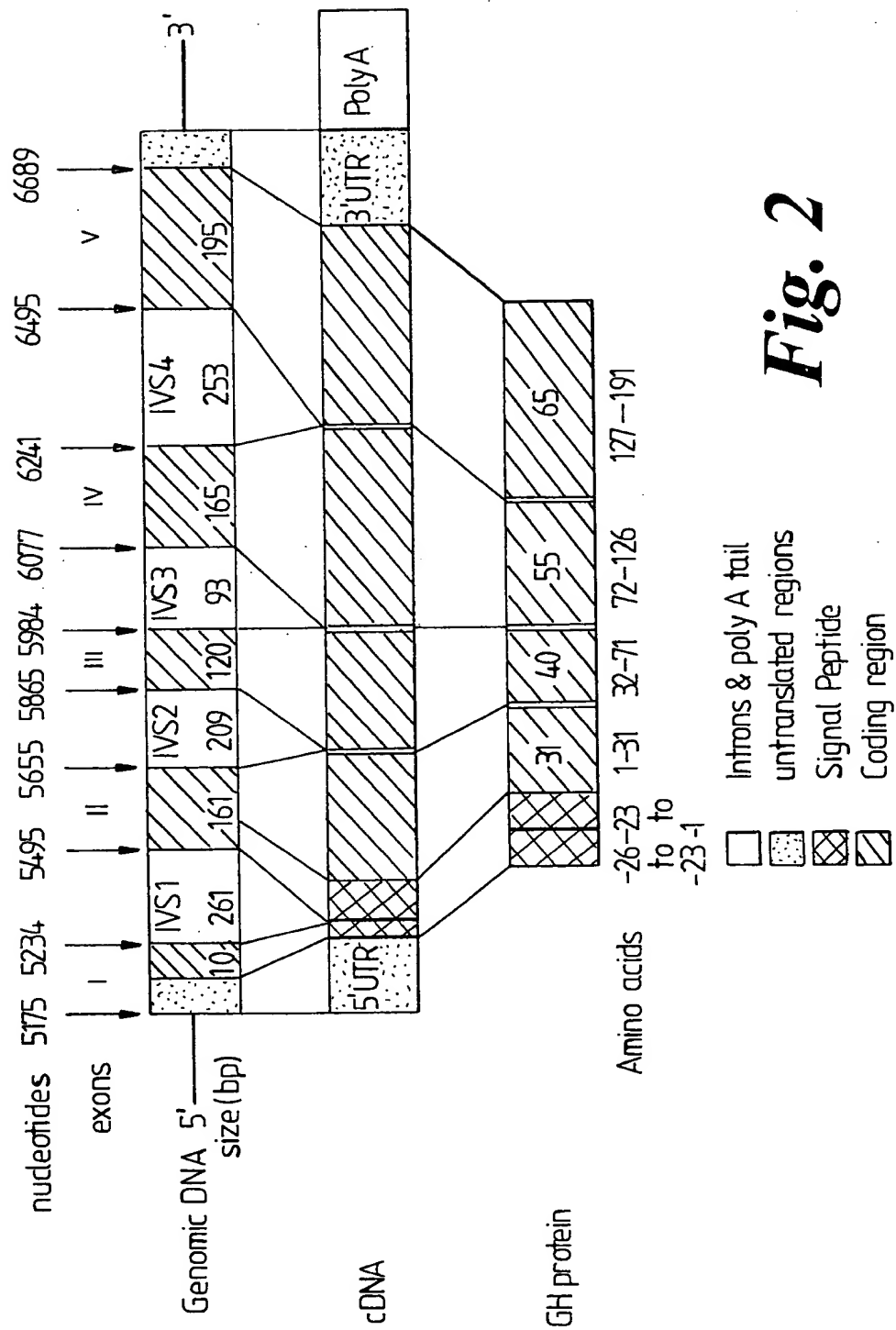


Fig. 2

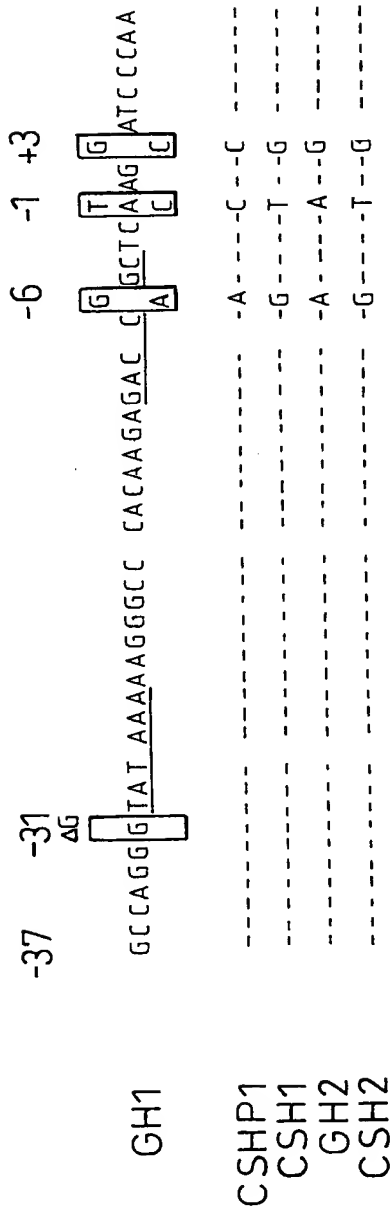
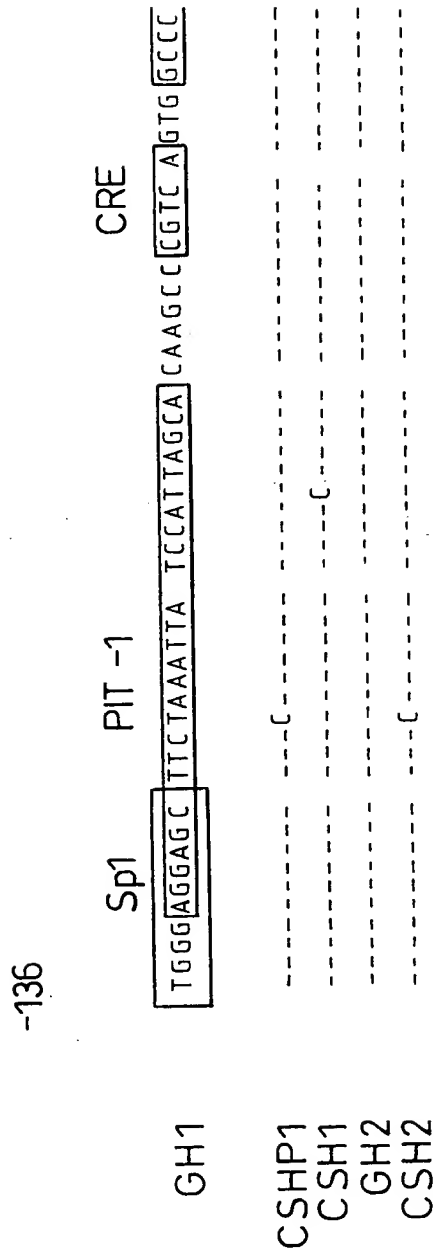


Fig. 3

GenBank

5 ttcctgccccacatgccaaacagcaccatgaggcaacaccattcttaacctctcagtgaccaaggctcctcat 1501-1575
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 tttcgtaaaaatagaaataagcccaatagcgcgtttttttgtgtgttttctggtggtttttctgagacaagatct 1576-1650
 aaagcattttatctttatcgggttatcgcgcaaaaaaacacaacaaagacccccaaaaagactctgttctaga
 tgctctgtgtgccaggctggagtgagtgagtggtgcaatctccattcacggcaacctctgccacctggactcaagtga 1651-1725
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 10 ttcacccacctcagcctcccgagtagctgggactacaggtcatgctactacacctgggtaactctgtgtatttctt 1726-1800
 aagtgggtggagtcggagggtcatcgacctgatgtccagtagatgtggaccgattagacacataaagaa
 gtagagacaggttttactatgttggccaggctggtctcaaaactcctgagctcaagcgatccacccgcctcagcct 1801-1875
 catctctgtccaaatgatacaacgggtccgaccagagtttgaggactcaggttcgctaggtgggaggagtcgga
 15 cccaaagtgtgggattacaggcgtgagccactgcggccggcccaacagtcggttggtcgaaaggcagctgtgc 1876-1950
 gggtttcacgaccctaattgccgactcgtgacgcggggccgggtgtgtcacgcaaccagcttcccgctcgacacg
 20 acattgaaggccatcctgcattctgaggtacttgggaatgtggtggacggcacgcccctgaggaaggcgaggagtg 1951-2025
 tgtaactccggtaggacgtagactccatgaaccacttacaccacctgccgtgcgggactcctcccgctcctcac
 cgagg 2026-2030
 gctcc
 25 PCR primers are marked in bold (42-1984 = 1942bp).
 Sequencing primers are underlined (GHLR3.1, 541-558; GHLR3.2, 1006-1023; GHLR3.3, 1422-1440;
 GHLR5.0, 640-658)

Figure 5

	-700	ctgttttcttg	gtttgtgtct	ctgctgcaag	tccaaggagc	tggggcaata	-651
5	-650	ccttgagtct	gggttcttcg	tccccaggga	cctgggggag	ccccagcaat	-601
	-600	gctcagggaa	aggggagagc	aaagtgtggg	gttggttctc	tctagtggtc	-551
	-550	agtgttgga	ctgcatccag	ctgactcagg	ctgacccagg	agtcctcagc	-501
	-500	agaagtggaa	ttcaggactg	aatcgtgctc	acaacccccca	caatctattg	-451
	-450	gctgtgcttg	gccccctttc	ccaacacaca	cattctgtct	ggtgggtgga	-401
10	-400	ggttaaacat	gcggggagga	ggaaagggat	aggatagaga	atgggatgtg	-351
	-350	gtcggtaggg	ggtctcaagg	actggctatc	ctgacatcct	tctccgcgtt	-301
	-300	caggttggcc	accatggcct	gcggccagag	ggcaccacag	tgacccttaa	-251
	-250	agagaggaca	agttgggtgg	tatctctggc	tgacactctg	tgacacaacc	-201
	-200	tcacaacact	ggtgacgggt	ggaaggga	gatgacaagc	cagggggcat	-151
15	-150	gatcccagca	tgtgtgggag	gagcttctaa	attatccatt	agcacaagcc	-101
	-100	cgtcagtggc	cccatgcata	aatgtacaca	gaaacagggtg	gggggagacag	-51
	-50	tgggagagaa	ggggccagggt	tataaaaagg	gcccacaaga	gaccagctca	-1
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	+51	cacctagcgg	caATGGCTAC	AGgttaagcgc	ccctaaaatc	cctttgggca	+100
20	+101	caatgtgtcc	tgaggggaga	ggcagcgacc	tgtagatggg	acggggggcac	+150
	+151	taaccctcag	gtttggggct	tctgaatgtg	agtatcgcca	tgtaagccca	+200
	+201	gtatattggcc	aatctcagaa	agctcctggt	ccctggagggt	atggagagag	+250
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	+351	TGCTGGCTTT	TGGCCTGCTC	TGCCTGCCCT	GGCTTCAAGA	GGGCAGTGCC	+400
	+401	TTCCCAACCA	TTCCCTTATC	CAGGCTTTTT	GACAACGCTA	TGCTCCGCGC	+450
	+451	CCATCGTCTG	CACCAGCTGG	CCTTTGACAC	CTACCAGGAG	TTTgtaagct	+500
	+501	cttgggggaat	gggtgcgcac	caggggtggc	aggaaggggt	gactttcccc	+550
	+551	cgctgggaaa	taagaggagg	agactaagga	gctcagggtt	tttcccgaa	+600
30	+601	cgaaaaatgca	ggcagatgag	cacacgctga	gtgaggttcc	cagaaaagta	+650
	+651	acaatgggag	ctggtctcca	gcgtagacct	tggtgggagg	tccttctcct	+700
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	+751	CCCCAGACCT	CCCTCTGTTT	CTCAGAGTCT	ATTCCGACAC	CCTCCAACAG	+800
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	+1051	TAGAGGAAGG	CATCCAAACG	CATCTGGGGg	tgaggggtggc	gccaggggtc	+1100
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	+1201	cttcatttcc	cctcgtgaat	cctccaggcc	tttctctaca	ccctgaagggt	+1250
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	+1451	TCAGGAAGGA	CATGGACAAG	GTGAGACAT	TCCTGCGCAT	CGTGCAGTGC	+1500
	+1501	CGCTCTGTGG	AGGGCAGCTG	TGGCTTCTAG	ctgcccgggt	ggcatcctctg	+1550
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	+2251	ttccaaattc	gaaatttcta	tttaaccatt	atatattttac	ttgtttgcta	+2300

Figure 5 (continued)

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[illegible]

Figure 6

Growth hormone 1
 5 Gene symbol : *GHI*
 Location : 17q

1 2

-26 ATG GCT ACA G↓GC TCC CGG ACG TCC CTG CTC CTG GCT TTT GGC CTG -12
 Met Ala Thr G ly Ser Arg Thr Ser Leu Leu Leu Ala Phe Gly Leu

10 -11 CTC TGC CTG CCC TGG CTT CAA GAG GGC AGT GCC TTC CCA ACC ATT 4
 Leu Cys Leu Pro Trp Leu Gln Glu Gly Ser Ala Phe Pro Thr Ile

15 5 CCC TTA TCC AGG CTT TTT GAC AAC GCT AGT CTC CGC GCC CAT CGT 19
 Pro Leu Ser Arg Leu Phe Asp Asn Ala Ser Leu Arg Ala His Arg

20 CTG CAC CAG CTG GCC TTT GAC ACC TAC CAG GAG TTT↓GAA GAA GCC 34
 Leu His Gln Leu Ala Phe Asp Thr Tyr Gln Glu Phe Glu Glu Ala

20 35 TAT ATC CCA AAG GAA CAG AAG TAT TCA TTC CTG CAG AAC CCC CAG 49
 Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn Pro Gln

50 ACC TCC CTC TGT TTC TCA GAG TCT ATT CCG ACA CCC TCC AAC AGG 64
 Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn Arg

25 65 GAG GAA ACA CAA CAG AAA TCC↓AAC CTA GAG CTG CTC CGC ATC TCC 79
 Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser

80 CTG CTG CTC ATC CAG TCG TGG CTG GAG CCC GTG CAG TTC CTC AGG 94
 Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe Leu Arg

95 AGT GTC TTC GCC AAC AGC CTG GTG TAC GGC GCC TCT GAC AGC AAC 109
 Ser Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser Asn

35 110 GTC TAT GAC CTC CTA AAG GAC CTA GAG GAA GGC ATC CAA ACG CTG 124
 Val Tyr Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu

125 ATG GGG↓AGG CTG GAA GAT GGC AGC CCC CGG ACT GGG CAG ATC TTC 139
 Met Gly Arg Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe

40 140 AAG CAG ACC TAC AGC AAG TTC GAC ACA AAC TCA CAC AAC GAT GAC 154
 Lys Gln Thr Tyr Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp

45 155 GCA CTA CTC AAG AAC TAC GGG CTG CTC TAC TGC TTC AGG AAG GAC 169
 Ala Leu Leu Lys Asn Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp

170 ATG GAC AAG GTC GAG ACA TTC CTG CGC ATC GTG CAG TGC CGC TCT 184
 Met Asp Lys Val Glu Thr Phe Leu Arg Ile Val Gln Cys Arg Ser

50 185 GTG GAG GGC AGC TGT GGC TTC TAG
 Val Glu Gly Ser Cys Gly Phe *

5 Location : 17q

		1 2		
	-26	ATG GCT ACA G↓GC TCC CGG ACG TCC CTG CTC CTG GCT TTT GGC CTG	-12	
		Met Ala Thr G ly Ser Arg Thr Ser Leu Leu Leu Ala Phe Gly Leu		
10	-11	CTC TGC CTG CCC TGG CTT CAA GAG GGC AGT GCC TTC CCA ACC ATT	4	
		Leu Cys Leu Pro Trp Leu Gln Glu Gly Ser Ala Phe Pro Thr Ile		
	5	CCC TTA TCC AGG CTT TTT GAC AAC GCT AGT CTC CGC GCC CAT CGT	19	
		Pro Leu Ser Arg Leu Phe Asp Asn Ala Ser Leu Arg Ala His Arg		
15	20	CTG CAC CAG CTG GCC TTT GAC ACC TAC CAG GAG TTT ↓ GGG GAA GCC	34	
		Leu His Gln Leu Ala Phe Asp Thr Tyr Gln Glu Phe Gly Glu Ala		
	35	TAT ATC CCA AAG GAA CAG AAG TAT TCA TTC CTG CAG AAC CCC CAG	49	
20		Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn Pro Gln		
	50	ACC TCC CTC TGT TTC TCA GAG TCT ATT CCG ACA CCC TCC AAC AGG	64	
		Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn Arg		
25	65	GAG GAA ACA CAA CAG AAA TCC ↓ AAC CTA GAG CTG CTC CGC ATC TCC	79	
		Glu Glu Thr Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser		
	80	CTG CTG CTC ATC CAG TCG TGG CTG GAG CCC GTG CAG TTC CTC AGG	94	
		Leu Leu Leu Ile Gln Ser Trp Leu Glu Pro Val Gln Phe Leu Arg		
30	95	AGT GTC TTC GCC AAC AGC CTG GTG TAC GGC GCC TCT GAC AGC AAC	109	
		Ser Val Phe Ala Asn Ser Leu Val Tyr Gly Ala Ser Asp Ser Asn		
	110	GTC TAT GAC CTC CTA AAG GAC CTA GAG GAA GGC ATC CAA ACG CTG	124	
35		Val Tyr Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu		
	125	ATG GGG ↓ AGG CTG GAA GAT GGC AGC CCC CGG ACT GGG CAG ATC TTC	139	
		Met Gly Arg Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe		
40	140	AAG CAG ACC TAC AGC AAG TTC GAC ACA AAC TCA CAC AAC GAT GAC	154	
		Lys Gln Thr Tyr Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp		
	155	GCA CTA CTC AAG AAC TAC GGG CTG CTC TAC TGC TTC AGG AAG GAC	169	
		Ala Leu Leu Lys Asn Tyr Gly Leu Leu Tyr Cys Phe Arg Lys Asp		
45	170	ATG GAC AAG GTC GAG ACA TTC CTG CGC ATC GTG CAG TGC CGC TCT	184	
		Met Asp Lys Val Glu Thr Phe Leu Arg Ile Val Gln Cys Arg Ser		
	185	GTG GAG GGC AGC TGT GGC TTC TAG		
50		Val Glu Gly Ser Cys Gly Phe *		

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3000000
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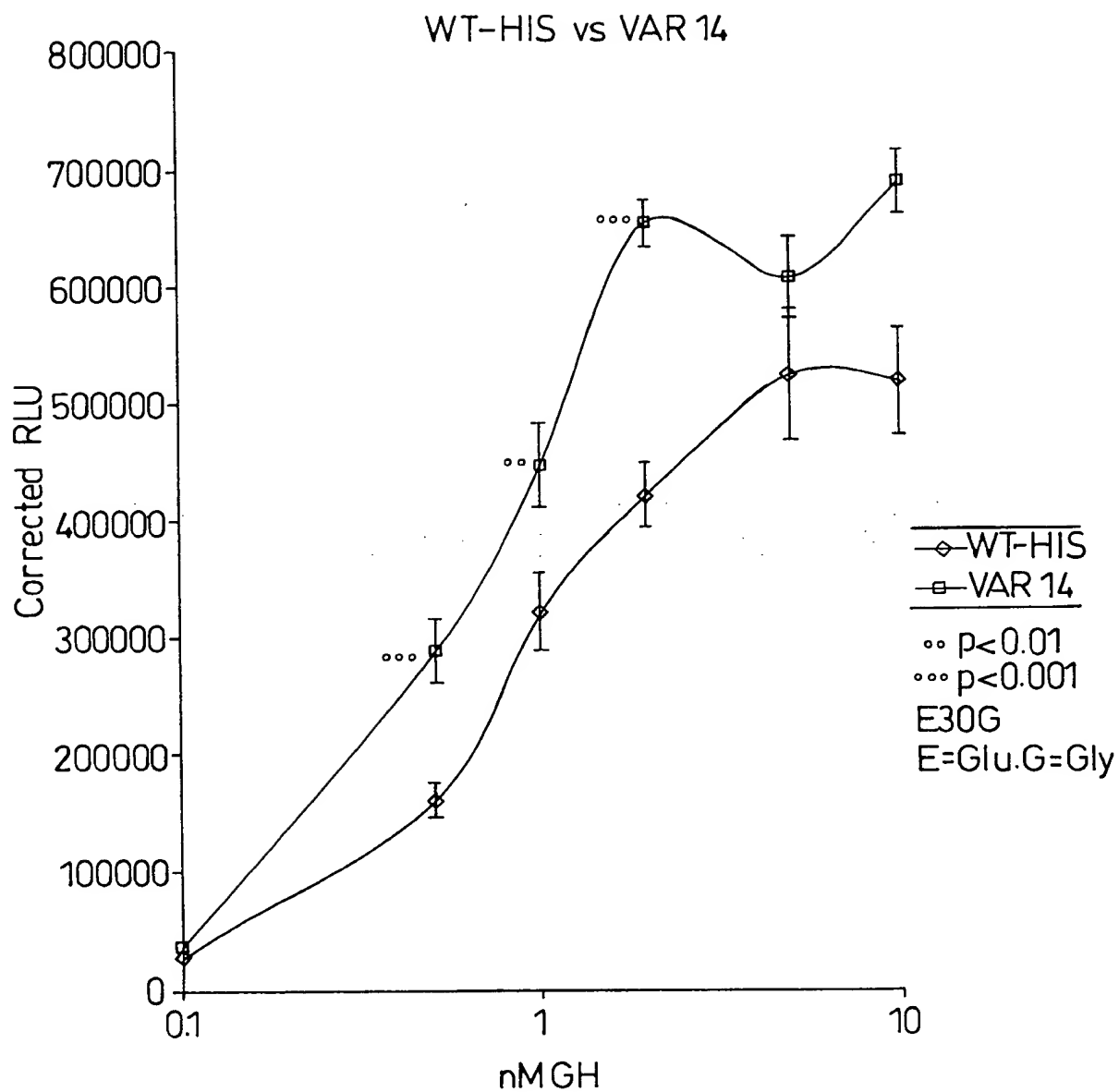


Fig. 8